AMENDMENTS TO THE SPECIFICATION.

After the abstract, please delete the existing sequence listing and insert the accompany sequence listing (pages 1-93).

At page 9, amend paragraph 0028 as follows:

[0028] In this regard, the first general step of linker design involves identification of plausible sites to be linked. Appropriate linkage sites on each of the V_H and V_L polypeptide domains include those which will result in the minimum loss of residues from the polypeptide domains, and which will necessitate a linker comprising a minimum number of residues consistent with the need for molecule stability. A pair of sites defines a "gap" to be linked. Linkers connecting the C-terminus of one domain to the N-terminus of the next generally comprise hydrophilic amino acids which assume an unstructured configuration in physiological solutions and preferably are free of residues having large side groups which might interfere with proper folding of the V_H and V_L chains. Thus, suitable linkers under the invention generally comprise polypeptide chains of alternating sets of glycine and serine residues, and may include glutamic acid and lysine residues inserted to enhance solubility. One particular linker under the invention has the amino acid sequence $[(Gly)_4Ser]_3$ (SEQ ID NO:1). Another particularly preferred linker has the amino acid sequence comprising 2 or 3 repeats of $[(Ser)_4Gly]$ (SEQ ID NO:2) such as $[(Ser)_4Gly]_3$ (SEQ ID NO:3). Nucleotide sequences encoding such linker moieties can be readily provided using various oligonucleotide synthesis techniques known in the art. *See, e.g.,* Sambrook, *supra.*

At pages 44-45, amend paragraph 0162 as follows:

[0162] To construct the vector pSYN3, a 1.5 kb stuffer fragment was amplified from pCANTAB5E (Pharmacia Biotech, Milwaukee, WI.) using PCR with the primers LMB3 (Marks, *et al.* (1991) *Eur. J. Immunol.* 21:985-991) and E-tagback (5'-ACC ACC GAA TTC TTA TTA ATG GTG ATG ATG GTG GAT GAC CAG CCG GTT CCA GCG G-3', ~~(SEQ ID NO:1)~~ (SEQ ID NO:4). The DNA fragment was digested with S*fi*I *and Notf,* gel purified, and ligated into pCANTAB5E digested with S*fi*I *and* NotI. Ligated DNA was used to transform *Escherichia coli* TG1 (Gibson (1991) *Studies on the Epstein-Barr virus genome. University of Cambridge, Cambridge, U. K.*), and clones containing the correct insert were identified by DNA sequencing.

The resulting vector permits subcloning of phage-displayed scFv as *SfiI-NotI or McoI-NotI* fragments for secretion into the periplasm of *E. coli* as native scFv with a C-terminal E epitope tag followed by a hexahistidine tag.

At pages 46-47, amend Table 1 as follows:

Table 1. Oligonucleotide primers used for PCR of mouse immunoglobulin genes.

Primer ID	Sequence	Seq I.D. No.
A. 1st strand cDNA synthesis		
Mouse heavy chain constant region primers		
MIgG1/2 For	5′ CTG GAC AGG GAT CCA GAG TTC CA 3′	~~1~~ 5
MIgG3 For	5′ CTG GAC AGG GCT CCA TAG TTC CA 3′	~~2~~ 6
Mouse □ constant region primer		
MC_KFor	5′ CTC ATT CCT GTT GAA GCT CTT GAC 3′	~~3~~ 7
B. Primary PCR		
Mouse V_H back primers		
VH1 Back	5′ GAG GTG CAG CTT CAG GAG TCA GG 3′	~~4~~ 8
VH2 Back	5′ GAT GTG CAG CTT CAG GAG TCR GG 3′	~~5~~ 9
VH3 Back	5′ CAG GTG CAG CTG AAG SAG TCA GG 3′	~~6~~ 10
VH4/6 Back	5′ GAG GTY CAG CTG CAR CAR TCT GG 3′	~~7~~ 11
VH5/9 Back	5′ CAG GTY CAR CTG CAG CAG YCT GG 3′	~~8~~ 12
VH7 Back	5′ GAR GTG AAG CTG GTG GAR TCT GG 3′	~~9~~ 13
VH8 Back	5′ GAG GTT CAG CTT CAG CAG TCT GG 3′	~~10~~ 14
VH10 Back	5′ GAA GTG CAG CTG KTG GAG WCT GG 3′	~~11~~ 15
VH11 Back	5′ CAG ATC CAG TTG CTG CAG TCT GG 3′	~~12~~ 16
Mouse V_H back primers		
VH1 Back	5′ GAC ATT GTG ATG WCA CAG TCT CC 3′	~~13~~ 17
VH2 Back	5′ GAT GTT KTG ATG ACC CAA ACT CC 3′	~~14~~ 18
VH3 Back	5′ GAT ATT GTG ATR ACB CAG GCW GC 3′	~~15~~ 19
VH4 Back	5′ GAC ATT GTG CTG ACM CAR TCT CC 3′	~~16~~ 20
VH5 Back	5′ SAA AWT GTK CTC ACC CAG TCT CC 3′	~~17~~ 21
VH6 Back	5′ GAY ATY VWG ATG ACM CAG WCT CC 3′	~~18~~ 22
VH7 Back	5′ CAA ATT GTT CTC ACC CAG TCT CC 3′	~~19~~ 23
VH8 Back	5′ TCA TTA TTG CAG GTG CTT GTG GG 3′	~~20~~ 24
Mouse Jh forward primers		

JH1 For 5' TGA GGA GAC GGT GAC CGT GGT CCC 3' ~~21~~ 25
JH2 For 5' TGA GGA GAC TGT GAG AGT GGT GCC 3' ~~22~~ 26
JH3 For 5' TGC AGA GAC AGT GAC CAG AGT CCC 3' ~~23~~ 27
JH4 For 5' TGA GGA GAC GGT GAC TGA GGT TCC 3' ~~24~~ 28

Mouse Jκ forward primers:
Jκ1 For 5' TTT GAT TTC CAG CTT GGT GCC TCC 3' ~~25~~ 29
Jκ2 For 5' TTT TAT TTC CAG CTT GGT CCC CCC 3' ~~26~~ 30
Jκ3 For 5' TTT TAT TTC CAG TCT GGT CCC ATC 3' ~~27~~ 31
Jκ4 For 5' TTT TAT TTC CAA CTT TGT CCC CGA 3' ~~28~~ 32
Jκ5 For 5' TTT CAG CTC CAG CTT GGT CCC AGC 3' ~~29~~ 33

C. Reamplification primers containing restriction sites
Mouse VH Sfi back primers

VH1 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTG CAG CTT CAG GAG TCA GG 3' ~~30~~ 34
VH2 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAT GTG CAG CTT CAG GAG TCR GG 3' ~~31~~ 35
VH3 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG GTG CAG CTG AAG SAG TCA GG 3' ~~32~~ 36
VH4/6 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTY CAG CTG CAR CAR TCT GG 3' ~~33~~ 37
VH5/9 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG GTY CAR CTG CAG CAG YCT GG 3' ~~34~~ 38
VH7 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAR GTG AAG CTG GTG GAR TCT GG 3' ~~35~~ 39
VH8 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAG GTT CAG CTT CAG CAG TCT GG 3' ~~36~~ 40
VH10 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC GAA GTG CAG CTG KTG GAG WCT GG 3' ~~37~~ 41
VH11 Sfi 5' GTC CTC GCA ACT GCG GCC CAG CCG GCC ATG GCC CAG ATC CAG TTG CTG CAG TCT GG 3' ~~38~~ 42

3 Mouse Jκ Not forward primers
6

Jκ1 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT GAT TTC CAG CTT GGT GCC TCC 3' ~~39~~ 43
Jκ2 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT TAT TTC CAG CTT GGT CCC CCC 3' ~~40~~ 44
Jκ3 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT TAT TTC CAG TCT GGT CCC ATC 3' ~~41~~ 45
Jκ4 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT TAT TTC CAA CTT TGT CCC CGA 3' ~~42~~ 46
Jκ5 Not 5' GAG TCA TTC TCG ACT TGC GGC CGC TTT CAG CTC CAG CTT GGT CCC AGC 3' ~~43~~ 47

R = A/G, Y = C/T, S = G/C, K = G/T, W = A/T, M = A/C, V = C/G/A, B = G/C/T, and H = C/A/T.

At pages 47-48, amend paragraph 0166 as follows:

[0001] scFv gene repertoires were assembled from purified V_H and V_K gene repertoires and linker DNA by using splicing by overlap extension. Linker DNA encoded the peptide sequence (G_4S_3, SEQ ID NO:~~45~~ 278) Huston, *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883) and was complementary to the 3' ends of the rearranged V_H genes and the 5' ends of the rearranged V. genes. The V_H and V_K DNAs (1.5 μg of each) were combined with 500 ng of linker DNA (Recombinant Phage Antibody System; Pharmacia Biotech) in a 25 μl PCR mixture containing 250 μm (each) deoxynucteoside triphosphate, 1.5 mM MgCl, 10 μg of bovine serum albumin/ml, and 1 μl (5 U) of *Taq* DNA polymerase (Promega) in the buffer supplied by the manufacturer, and the mixture was cycled 10 times (at 94°C for 1 min, 62°C for 1 min, and 72°C for 1 min) to join the fragments. Flanking oligonucleotide primers (RS, provided in the Recombinant Phage Antibody System kit, for library I and an equimolar mixture of V_HSfi and JKNot primers [Table **1**] for library 2) were added, and the reaction mixture was cycled for 33 cycles (at 94°C for 1 min, 55°C for 1 min, and 72°C for 1 min) to append restriction sites.

At page57, replace Table 4 with the accompanying replacement Table 4 (4 pages).

At pages 63-64 amend paragraph 0198 as follows:

[0002] V_H genes of C25, S25, and 3D12 single-chain fragment variable (scFv) were amplified using PCR from the respective phagemid DNA with the primer pairs GTC TCC TGA GCT AGC TGA GGA GAC GGT GAC CGT GGT (SEQ ID NO:~~44~~ 96) and either GTA CCA ACG CGT GTC TTG TCC CAG GTC CAG CTG CAG GAG TCT (C25, SEQ ID NO:~~45~~ 97), GTA CCA ACG CGT GTC TTG TCC CAG GTG AAG CTG CAG CAG TCA (S25, SEQ ID NO:~~46~~ 98), or GTA CCA ACG CGT GTC TTG TCC CAG GTG CAG CTG GTG CAG TCT (3D12, SEQ ID NO:~~47~~ 99). DNA was digested with Mlu1 and *Nhe*I, ligated into N5KG1Val- Lark (gift of Mitch Reff, IDEC Pharmaceuticals, San Diego) and clones containing the correct V_H identified by DNA sequencing. V_genes of C25, S25, and 3D12 scFv were amplified from the respective phagemid DNA with the primer pairs TCA GTC GTT GCA TGT ACT CCA GGT GCA CGA TGT GAC ATC GAG CTC ACT CAG TCT (SEQ ID NO:~~48~~ 100) and CTG GAA ATC AAA CGT ACG TTT TAT TTC CAG CTT GGT (C25, SEQ ID NO:~~49~~ 101), TCA GTC GTT GCA TGT ACT CCA GGT GCA CGA TGT GAC ATC GAG CTC ACT CAG TCT (SEQ ID NO:~~50~~ 102) and CTG GAA

ATC AAA CGT ACG TTT GAT TTC CAG CTT GGT (S25, SEQ ID NO:~~51~~ 103), or TCA GTC GTT GCA TGT ACT CCA GGT GCA CGA TGT GAC ATC GTG ATG ACC CAG TCT (SEQ ID NO:~~52~~ 104) and CTG GAA ATC AAA CGT ACG TTT TAT CTC CAG CTT GGT (3D12, SEQ ID NO:~~53~~ 105), cloned into pCR-TOPO (Invitrogen) and clones containing the correct V_identified by DNA sequencing. V_genes were excised from pCR-TOPO with *Dra*III and *Bsi*WI and ligated into *Dra*III- and BsiWI-digested N5KG1Val-Lark DNA containing the appropriate V_H gene. Clones containing the correct V_H and V_K gene were identified by DNA sequencing, and vector DNA was used to transfect CHO DG44 cells by electroporation. Stable cell lines were established by selection in G418 and expanded into 1L spinner flasks. Supernatant containing IgG was collected, concentrated by ultrafiltration, and purified on Protein G (Pharmacia).

At pages 79-81, please amend Table 9 as follows:

Table 9. CDR 3-sequences and affinities for human scFv antibodies isolated from immune and non-immune libraries, selected on BoNT/A and BoNT/A H_C.[a]

Non-immune library Heavy Chain				
Clone	Family	Segment	Diff from Genome	V_H CDR3
2A9[b]	V_H3	DP54	5	GRGVN (SEQ ID NO:~~54~~ 106)
2B1[b]	V_H3	DP46	0	NGDPEAFDY (SEQ ID NO:~~55~~ 107)
2H6[b]	V_H3	DP47	6	ALQSDSPYFD (SEQ ID NO:~~56~~ 108)
3C2[b]	V_H3	DP46	2	DLAIFAGNDY (SEQ ID NO:~~57~~ 109)
2B6[b]	V_H3	DP47	3	VGVDRWYPADY (SEQ ID NO:~~58~~ 110)
3F6[c]	V_H3	DP47	2	DLLDGSGAYFDY (SEQ ID NO:~~59~~ 111)
2A2[b]	V_H3	DP46	0	DLDYGGNAGYFDL (SEQ ID NO:~~60~~ 112)
2B10[b]	V_H3	DP46	0	DLDYGGNAGYFDL (SEQ ID NO:~~61~~ 113)
2E6[b]	V_H3	DP46	0	DYTANYYYYGMDV (SEQ ID NO:~~62~~ 114)

3D1b	V_H3	DP47	7	DLGYGSGTSSYYLDY (SEQ ID NO:~~63~~115)
Non-immune library Light Chain				V_L CDR3
2A9[b]	Vκ1	L12A	6	QQANSFPRT (SEQ ID NO:~~64~~116)
2B1[b]	Vκ1	L1	11	LQDYNGWT (SEQ ID NO:~~65~~117)
2H6[b]	Vλ3	DPL16	7	NSRDSSGNHVV (SEQ ID NO:~~66~~118)
3C2[b]	Vλ3	DPL16	9	KSRDSRGNHLAL (SEQ ID NO:~~67~~119)
2B6[b]	Vκ1	L12A	5	QQYHTISRT (SEQ ID NO:~~68~~120)
3F6[c]	Vλ3	DPL16	3	NSRDSSGNHVV (SEQ ID NO:~~69~~121)
2A2[b]	Vλ3	DPL16	10	HSRDSSVTNLD (SEQ ID NO:~~70~~122)
2B10[b]	Vλ3	DPL16	4	NSRDSSGNHQV (SEQ ID NO:~~71~~123)
2E6[b]	Vλ2	DPL12	14	NSRDSSGVV (SEQ ID NO:~~72~~124)
3D1[b]	Vλ3	DPL16	5	NSRDSSGNHVV (SEQ ID NO:~~73~~125)
Immune Library Heavy Chain				
Clone	Family	Segment	Diff from Genome	V_H CDR3
3B8[c]	V_H1	V1-2	10	LATYYYFGLDV (SEQ ID NO:~~74~~126)
3F10[c]	V_H1	V1-2	10	LATYYYFGLDV (SEQ ID NO:~~75~~127)
2B11[c]	V_H1	DP10	11	GPWELVGYFDS (SEQ ID NO:~~76~~128)
3A6c	V_H3	DP50	18	EPDWLLWGDRGALDV (SEQ ID NO:~~77~~129)
3D12[c]	V_H3	DP50	13	EPDWLLWGDRGALDV (SEQ ID NO:~~78~~130)
2A1[b]	V_H3	DP50	14	EPDWLLWGDRGALDV (SEQ ID NO:~~79~~131)
Immune Library Light Chain				
Clone	Family	Segment	Diff from	V_L CDR3

			Genome	
3B8 [c]	Vκ1	DPK7	12	QQYNSYVYT (SEQ ID NO:~~80~~ 132)
3F10 [c]	Vκ1	DPK8	10	QQLNSYPLT (SEQ ID NO:~~81~~ 133)
2B11 [c]	Vκ1	L12	11	QQLISYPLT (SEQ ID NO:~~82~~ 134)
3A6 [c]	Vκ1	L12	8	QHYNTYPYT (SEQ ID NO:~~83~~ 135)
3D12 [c]	Vκ1	L12	10	QHYNTYPYT (SEQ ID NO:~~84~~ 136)
2A1 [b]	Vκ1	L12	4	QHYNTYPYT (SEQ ID NO:~~85~~ 137)

[a] Human germline VH , Vκ and Vλ segments have been assigned as detailed in the V-BASE database (MRC Centre for Protein Engineering, Cambridge, UK). Listed clones, with identical VH or VL CDR 3 regions, showed different CDR 1, CDR 2 and framework regions, as indicated by their differences from the germline genes; accession can be made through GenBank with nos. AF090405–AF090420.
[b] Library selected on BoNT/A.
[c] Library selected on BoNT/A HC.

At pages 85-88, amend Table 11 as follows:

[0241] Table 11 amino acid sequences for affinity matured and/or modified antibodies.

Heavy Chains				
Clone	Framework 1	CDR1	Framework 2	CDR2
huC25	QVQLQESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO:~~86~~138)	DYYMY(SEQ ID NO:~~87~~139)	WVRQAPGKGLEWVA(SEQ ID NO:~~88~~140)	TISDGGSYTYYPDSVKG(SEQ ID NO:~~89~~141)
Ar1	QVQLQESGGGLVQPGGSLRLSCAASGFTFS (SEQ ID NO:~~90~~ 142)	DYYMY(SEQ ID NO:~~91~~ 143)	WVRQAPGKGLEWVA(SEQ ID NO:~~92~~144)	TISDGGSYTYYPDSVKG(SEQ ID NO:~~93~~145)
Ar2	QVQLQESGGGLVQPGGSLRLSCAASGFTFS(SEQ ID NO:~~94~~146)	DHYMY(SEQ ID NO:~~95~~147)	WVRQAPGKGLEWVA(SEQ ID NO:~~96~~148)	TISDGGSYTYYPDSVKG(SEQ ID NO:~~97~~149)
WR1(V)	QVQLQESGGGLVQPGGSLRLSCAASGFTSS (SEQ ID NO:~~98~~150)	DHYMY(SEQ ID NO:~~99~~151)	WVRQAPGKGLEWVA(SEQ ID NO:~~100~~152)	TISDGGSYTYYPDSVKG(SEQ ID NO:~~101~~153)
WR1(T)	QVQLQESGGGLVQPGGSLRLSCAASGFTSS (SEQ ID NO:~~102~~154)	DHYMY(SEQ ID NO:~~103~~155)	WVRQAPGKGLEWVA(SEQ ID NO:~~104~~156)	TISDGGSYTYYPDSVKG(SEQ ID NO:~~105~~157)
3D12	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS(SEQ ID NO:~~106~~158)	DYDMH(SEQ ID NO:~~107~~159)	WVRQAPGKGLEWVA(SEQ ID NO:~~108~~160)	VMWFDGTEKYSAESVKG(SEQ ID NO:~~109~~161)
3-1	QVQLVQSGGGVVHPGRSLKLSCAGSGFTFS(SEQ ID NO:~~110~~162)	DYDMH(SEQ ID NO:~~111~~163)	WVRQAPGKGLEWVA(SEQ ID NO:~~112~~164)	VMWFDGTEKYSAESVKG(SEQ ID NO:~~113~~165)

3-8	QVQLVQSGGGVVHPGRSLKLSC AGSGFTFS(SEQ ID NO:~~114~~166)	DYDMH(SEQ ID NO:~~115~~167)	WVRQAPGKGLEW VA(SEQ ID NO:~~116~~168)	VIWFDGTEKYSAE SVKG(SEQ ID NO:~~117~~169)
3-10	QVQLVQSGGGVVHPGRSLKLSC AGSGFTFS(SEQ ID NO:~~118~~170)	DYDMH(SEQ ID NO:~~119~~171)	WVRQAPGKGFEW VA(SEQ ID NO:~~120~~172)	VMWFDGTEKYSAE SVKG(SEQ ID NO:~~121~~173)
ING1	QVQLQQSGGGLVQPGGSLRLSC AASGFTFS(SEQ ID NO:~~122~~174)	NYAMT(SEQ ID NO:~~123~~175)	WVRQAPGKGLEW VS(SEQ ID NO:~~124~~176)	SISVGGSDTYYAD SVKG(SEQ ID NO:~~125~~177)
Heavy Chains cont'd				
	Framework 3	CDR3	Framework 4	
huC25	RFTISRDNSKNTLYLQMNSLRA EDTAMYYCSR(SEQ ID NO:~~126~~178)	YRYDDAMDY(S EQ ID NO:~~127~~179)	WGQGTLVTVSS (SEQ ID NO:~~128~~180)	
Ar1	RFTISRDNSKNTLYLQMNSLRA EDTAIYYCSR(SEQ ID NO:~~129~~181)	YRYDDAMDY(S EQ ID NO:~~130~~182)	WGQGTLVTVSS(SEQ ID NO:~~131~~183)	
Ar2	RFTTSRDNSKNTLYLQMNSLRA EDTAIYYCSR(SEQ ID NO:~~132~~184)	YRYDDAMDY(S EQ ID NO:~~133~~185)	WGQGTLVTVSS(SEQ ID NO:~~134~~186)	
WR1(V)	RFTVSRDNSKNTLYLQMNSLRA EDTAIYYCSR(SEQ ID NO:~~135~~187)	YRYDDAMDY(S EQ ID NO:~~136~~188)	WGQGTLVTVSS (SEQ ID NO:~~137~~189)	
WR1(T)	RFTTSRDNSKNTLYLQMNSLRA EDTAIYYCSR(SEQ ID NO:~~138~~190)	YRYDDAMDY(S EQ ID NO:~~139~~191)	WGQGTLVTVSS (SEQ ID NO:~~140~~192)	
3D12	RFTISRDNSKNTLFLQMNSLRA DDTAVYYCAR(SEQ ID NO:~~141~~193)	EPDWLLWGDRG ALDV(SEQ ID NO:~~142~~194)	WGQGTTVTVSS (SEQ ID NO:~~143~~195)	
3-1	RFTISRDNSKNTLFLQMNSLRA DDTAVYYCAR(SEQ ID NO:~~144~~196)	EPDWLLWGDRG ALDV(SEQ ID NO:~~145~~197)	WGQGTTVTVSS (SEQ ID NO:~~146~~198)	
3-8	RFTISRDNSKNTLFLQMNSLRA DDTAVYYCAR(SEQ ID NO:~~147~~199)	EPDWLLWGDRG ALDV(SEQ ID NO:~~148~~200)	WGQGTTVTVSS (SEQ ID NO:~~149~~201)	
3-10	RFTISRDNSKNTLFLQMNSLRA DDTAVYYCAR(SEQ ID NO:~~150~~202)	EPDRLLWGDRG ALDV(SEQ ID NO:~~151~~203)	WGQGTTVTVSS (SEQ ID NO:~~152~~204)	
ING1	RFTVSRDNSKNTLLLQMNSLRA EDTAVYYCAK(SEQ ID NO:~~153~~205)	VRTKYCSSLSC FAGFDS(SEQ ID NO:~~154~~206)	WGQGTLVTVSS (SEQ ID NO:~~155~~207)	
Light Chains				

Clone	Framework 1	CDR1	Framework 2	CDR2
huC25	EIVLTQSPATLSLSPGERATIS C(SEQ ID NO:~~156~~208)	RASESVDSYGH SFMQ(SEQ ID NO:~~157~~209)	WYQQKPGQAPRL LIY(SEQ ID NO:~~158~~210)	RASNLEP(SEQ ID NO:~~159~~211)
Ar1	EIVLTQSPATLSLSPGERATIS C(SEQ ID NO:~~160~~212)	RASESVDSYGH SFMQ(SEQ ID NO:~~161~~213)	WYQQKPGQAPRL LIY(SEQ ID NO:~~162~~214)	RASNLEP(SEQ ID NO:~~163~~215)
Ar2	EIVLTQSPATLSLSPGERATIS C(SEQ ID NO:~~164~~216)	RASESVDSYGH SFMQ(SEQ ID NO:~~165~~217)	WYQQKPGQAPRL LIY(SEQ ID NO:~~166~~218)	RASNLEP(SEQ ID NO:~~167~~219)
WR1(V)	EIVLTQSPATLSLSPGERATIS C(SEQ ID NO:~~168~~220)	RASESVDSYGH SFMQ(SEQ ID NO:~~169~~221)	WYQQKPGQAPRL LIY(SEQ ID NO:~~170~~222)	RASNLEP(SEQ ID NO:~~171~~223)
WR1(T)	EIVLTQSPATLSLSPGERATIS C(SEQ ID NO:~~172~~224)	RASESVDSYGH SFMQ(SEQ ID NO:~~173~~225)	WYQQKPGQAPRL LIY(SEQ ID NO:~~174~~226)	RASNLEP(SEQ ID NO:~~175~~227)
3D12	DIVMTQSPSTLSASVGDRVTIT C(SEQ ID NO:~~176~~228)	RASQSISSWLA (SEQ ID NO:~~177~~229)	WYQQKPGKAPKL LMY(SEQ ID NO:~~178~~230)	EASSLES(SEQ ID NO:~~179~~231)
3-1	DIVMTQSPSTLSASVGDRVTIT C(SEQ ID NO:~~180~~231)	WASQSISSRLA (SEQ ID NO:~~181~~233)	WYQQKPGKAPKL LMY(SEQ ID NO:~~182~~234)	EATSLGS(SEQ ID NO:~~183~~235)
3-8	DIVMTQSPSTLSASVGDRVTIT C(SEQ ID NO:~~184~~236)	RASQSISSWLA (SEQ ID NO:~~185~~237)	WYQQKPGKAPKL LMY(SEQ ID NO:~~186~~238)	GASSLGS(SEQ ID NO:~~187~~239)
3-10	DIVMTQSPSTLSASVGDRVTIT C(SEQ ID NO:~~188~~240)	RASQSISSWLA (SEQ ID NO:~~189~~241)	WYQQKPGKAPKL LMY(SEQ ID NO:~~190~~242)	EASSLGR(SEQ ID NO:~~191~~243)
ING1	DIVMTQSPSSLSASVGDRVTIT C(SEQ ID NO:~~192~~244)	RASQSISSYLN (SEQ ID NO:~~193~~245)	WYQQKPGKAPKL LIY(SEQ ID NO:~~194~~246)	AASSLQS(SEQ ID NO:~~195~~247)
Light Chains cont'd.				
Clone	Framework 3	CDR3	Framework 4	
huC25	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC(SEQ ID NO:~~196~~248)	QQSNEDPFT (SEQ ID NO:~~197~~249)	FGQGTKVEIKR (SEQ ID NO:~~198~~250)	
Ar1	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC(SEQ ID NO:~~199~~251)	QQGNEVPFT (SEQ ID NO:~~200~~252)	FGQGTKVEIKR (SEQ ID NO:~~201~~253)	
Ar2	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC(SEQ ID	QQGNEVPFT (SEQ ID	FGQGTKVEIKR (SEQ ID	

	NO:~~202~~254)	NO:~~203~~255)	NO:~~204~~256)	
WR1(V)	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC(SEQ ID NO:~~205~~257)	QQGNEVPFT (SEQ ID NO:~~206~~258)	FGQGTKVEIKR (SEQ ID NO:~~207~~259)	
WR1(T)	GIPARFSGSGSGTDFTLTISSL EPEDFAVYYC(SEQ ID NO:~~208~~260)	QQGNEVPFT (SEQ ID NO:~~209~~261)	FGQGTKVEIKR (SEQ ID NO:~~210~~262)	
3D12	GVPSRFSGSGSGTEFTLTISSL QPDDFAAYYC(SEQ ID NO:~~211~~263)	QHYNTYPYT (SEQ ID NO:~~212~~264)	FGQGTKLEIKR (SEQ ID NO:~~213~~265)	
3-1	GVPSRFSGSGSGTEFTLTISSL QPDDFAAYYC(SEQ ID NO:~~214~~266)	QHYDTYPYT (SEQ ID NO:~~215~~267)	FGQGTKLEIKR (SEQ ID NO:~~216~~268)	
3-8	GVPSRFSGSGSGTEFTLTISSL HPDDFAAYYC(SEQ ID NO:~~217~~269)	QHYNTYPYT(SEQ ID NO:~~218~~270)	FGQGTKLEIKR (SEQ ID NO:~~219~~271)	
3-10	GVPSRFSGSGSGTEFTLTISSL QPDDFAAYYC(SEQ ID NO:~~220~~272)	QHYSTYPYT(SEQ ID NO:~~221~~273)	FGQGTKLEIKR (SEQ ID NO:~~222~~274)	
ING1	GVPSRFSGSGSGTDFTLTISSL QPEDFATYYC(SEQ ID NO:~~223~~275)	QQSYSTPRTT(SEQ ID NO:~~224~~276)	FGGGTKVDIKR (SEQ ID NO:~~225~~277)	

*Sequence for complete heavy chain is heavy chain framework 1+ CDR1 + framework 2 + CDR2 + framework 3 + CDR3 + framework 4.

Sequence for complete light chain is light chain framework 1+ CDR1 + framework 2 + CDR2 + framework 3 + CDR3 + framework 4.

Table 4. Deduced protein sequences of VH and VL of BoNT/A Hc binding scFv classified by epitope recognized.

		Sequence[b]			
V_H Region					
Epitope 1		Framework 1 Framework 3	CDR 1 CDR3	Framework 2 Framework 4	CDR 2 Seq ID No
Clone	Lib[a]				
C15	1	QVKLQQSGAELVRPGASVKLSCKTSGYSFT MATLTVDKSSSTAYMQLSSPTSEDSAVYYCAR	SYWMN GIYYDYDGGNYYAMDY	WVKQGPGQGLEWIG WGQGTTVTASS	MIHPSNSEIRFNQKFED 48
C9	1	QVKLQQSGAELVRPGASVKLSCKTSGYSFT MATLTVDKSSSTAYMQLSSPTSEDSAVYYCAR	SYWMN GIYYvYDGGNTTAMDY	WVKQGPGQGLEWIG WGQGTTVTvSS	MIHPSNSEIRFNQKFEn 49
1D5	2	eVKLveSGAELVRPGASVnLSCKaSGYSFT kATLTVDKSSSTAYMQLSSPTSEDSAVYYCAR	SYWMN GIYYDYDeGyYYtlDY	WVKQrPGQGLEWIG WGQGTTlTvSS	MIHPSNSEtRlNQKFkD 50
C1	1	QVKLQQSGAELVRPGASVKLSCKaSGYSFT kATLTVDrSSSTAihQLSSPTSEDSAVYYCAR	SYWMN GlYgygf wyfdv	WVKQrPGQGLEWIG WGQGTTVTvSS	MIHPSNSdtRFNQKFED 51
S25	1	QVKLQQSGAELVRPGASVKLSCKaSGYSlT kATLTVDtSSSTAYMQLSSPTSEDSAVYYCAR	SYWMN GlYngf wyfDv	WVKQrPGQGLEWIG WGQGTTVTvSS	MIHPSdSdtRFNQKFED 52
1B6	2	QVqLQQSGAELVRPGvSVKiSCKaSGYtFi kATLTVDKSSnTAYMeLarlTSdDSAiYYCAR	DYAMH Rgkg AMDY	WVKQsPaksLEWIG WGQGTTVTvSS	vIssyygdtdyNQiFkg 53
1C9	2	QVqLkQSGAELVRPGvSVKiSCKaSGYtFi kATLTVnKSSnTAYMeLprlTSEDSAiYYCAR	DYAVH Rgkg AMDY	WVKQshaksLEWIG WGQGTsVTvSS	vIstyygdadyNpkFkg 54
1E8	2	eVqLQeSGpgLVkPsqSlsLtCtvtGYSiT risiTrDtSknqfflQLnSvTtEDtgtYYCAR	dYawN Gyd AMDY	WirQfPGkkLEWmG WGQGTsVTvSS	yIs ysgstgynpslks 55
1G7	2	eVqLQeSGpgLVkPsqSlsLtCtvtGYSiT risiTrDtSknqfflQLnSvTtEDtgtYYCAR	dYawy Gyd AMDY	WirQfPGkkLEWmG WGQGTsVTvSS	yIs ysgstgynpslks 56
Epitope 2					
1A1	2	EVKLVESGGGLVQPGGSRKLSCATSGFTFS RFTISRDNAKNTLYLQMSSLKSEDTAMYYCVR	DYYMS HGYGNYPSH WYFDV	WIRQSPDKRLEWVA WGAGTTVTVSS	TISDGGTYTYYPDSVKG 57
1F1	2	EVKLVESGGGLVQPGGSLKlSCAaSGFTFS RvTISRDNAKsTLYLQMSSLqSEDTAMYlCtR	nYgMS HGYGNYPSy WYFDV	WvRQtPDKRLEWVA WGAGTTVTVSS	mISsGGsYnYYsDSVKG 58
C39	1	qVqLqESGGGsVkPGGSlKLSCAaSGFTFS RFTISRDNAKNnLYLQMSSLKSEDTAiYYCVR	DYYMS yrYdegl Dy	WvRQtPeKRLEWVA WGqGTTVTVSS	TISDGGsYTYYPDSVKG 59
C25	1	qVqLqESGGGLVkPGGSlKLSCAaSGFTFS RFTISRDNAKNnLYLQMSSLKSEDTAMYYCsR	DYYMy YrYddam Dy	WvRQtPeKRLEWVA WGqGTTVTVSS	TISDGGsYTYYPDSVKG 60
2G5	2	EVKLVESGGGLVkPGGSlKLSCAaSGFTFS RFTISRDNAKhnLYLQMShLKSEDTAMYYCaR	sYaMS nlpydhv Dy	WvRQtPeKRLEWVA WGqGTsVTVSS	TISDGGTYTYYtDnVKG 61
3C3	2	EVKLkESGGGLVkPGGSlKLSCAaSGFTFS	sYaMS	WvRQtPeKRLEWVA	TISDGGTYTYYtDnVKG

		RFTISRDNAKhnLYLQMShLKSEDTAMYYCaR	nlpydhv Dy	WGqGTsVTVSS	62
3F4	2	hgKLVESGGGLVkPGGSlKLSCAaSGFTFS RFTISRDNAKhnLYLQMShLKSEDTAMYYCaR	sYaMS nlpydhv Dy	WvRQtPehRLEWVA WGqGTsVTVSS	TISDGGTfTYYtDnVKG 63
3H4	2	EVKLVESGGGLVkPGGplKLSCAaSGFTFS	sYaMS	WvRQtPehRLEWVA	TISDGGTfTYYtDnVKG
		RFTISRDNAKhnLYLQMShLKSEDTAMYYCaR	nlpydhv Dy	WGqGTsVTVSS	64
Epitope 3					
1B3	2	EVQLQESGGGVVQPGRSLRLSCAASGFTFS RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	SYAMH DWSEGYYYYG MDV	WVRQAPGKGLEWVA WGQGTTVIVSS	VISYDGSNKYYADSVKG 65
1C6	2	qiQLlqSGGGVVQPGRSLRLSCAASGFTFS RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	SYAMH DWSEGYYYYG MDV	WVRQAPGKGLEWVA WGQGTTVIVSS	VISYDGSNKYYADSVKG 66
2B6	2	vklvesgpGlVkpsqslsltctvtgysitS RisitRDtSKNqffLklNSvtsEDTAtYYCAR	dYawn AgdgyYvd wyfdv	WiRQfPGnkLEWmg WGtGTTVIVSS	yInYDGSNnYnp SlKn 67
1G5	2	qVQLQqSGaelVQPGaSvkmSCkASGyTFt kaTltvDtSssTaYmQlsSLtsEDsAVYYCAR	dYwtt Elgd aMDy	WVkQrPGqGLEWig WGQGTsVIVSS	dIypgsgstnynekfKs 68
1H6	2	EVQLQqSGaelVQPGaSvkmSCkASGyTFt kaTltvDtSssTaYmQlsSLtsEDsAVYYCAR	dYwtt Elgd aMDy	WVkQrPGqGLEWig WGQGTsVIVSS	dIypDsgstnynekfKs 69
Epitope 4					
1F3	2	EVQLQQSGAELVKPGASVKLSCKASGYTFT KATLTVDKPSSTAYMELSSLTSEDSAVYYCAR	SFWMH EAYGYWN FDV	WVKQRPGRGLEWIG WGTGTTVTVSS	RLDPNSGETKYNEKFKS 70
2E8	2	EVQLQQSGAELVKPGASVKLSCKASGYTFT	SFWMH	WVKQRPGRGLEWIG	RLDPNSGETKYNkKFKS
		KATLTVDKPSSTAYMELSSLTSEDSAVYYCAR	EAYGYWN FDV	WGTGTTVTVSS	71

V^L Region Epitope 1					
Clone	Lib	Framework 1 Framework 3	CDR 1 CDR 3	Framework 2 Framework 4	CDR 2 Seq ID NO
C15	1	DIELTQSPAIMSASPGEKVIMTC QVPIRFSGSGSGTSYSLTISRMEAEDSATYYC	SASS SVSHMY QQWSSYPFT	WYQQKPGSSPRLLIY FGSGTKLELKR	DTSNLAS 72
C9	1	DIdLTQSPAIMSsSPGEKVIiTC QVPaRFSGSGSGTSYSLTISsvEAEDaATYYC	SASS SVSyMh QQySgYPlT	WfQQKPGtSPkpwIY FGaGTKLEiKR	sTSNLAS 73
1D5	2	DIELTQSPAIMaASPGEKVIiTC QVPvRFSGSGSGTSYSLTISsMEAEDaATYYC	SASSs iSsSnlh QQWgSYPlT	WYQQKsetspkpwIY FGgGTKLEiKR	gTSNLAS 74
C1	1	DIELTQSPAIMSASPGEKVIMTC QVPvRFSGSGSGTSYSLTISRMEAEDaATYYC	SASS SVSyMY QQWSSYPlT	WYQQKPGSSPRLLIY FGaGTKLELKR	DTSNLAS 75
S25	1	DIELTQSPAlMaASPGEKVIiTC QVPvRFSGSGSGTSYSLTISsMEAEDaATYYC	SvSSs iSsSnlh QQWSSYPlT	WYQQKsGtSPkpwIY FGaGTKLEiKR	gTSNLAS 76
1B6	2	DIELTQSPAslavSlGqraIisC	raYesvdsygnSfMh	WYQQKPGqpPkLLIY	raSNLeS

		QiPaRFSGSGSrTdftLTinpvEAdDvATYYC	QQsnedPpT	FGaGTKLELKR	77
1C9	2	DIELTQSPAslavSlGqraIisC QiPaRFSGSGSrTdftLTInpvEAdDvATYYC	raYesvdsygnSfMh QQsnedPyT	WYQQKPGqpPkLLIY FGaGTKLEiKR	raSNLeS 78
1E8	2	DIELTQSPAIMSASPGEKVIMTC QVPaRFSGSGSGTSYSLTISsMEAEDaATYYC	SASS SVSyMh QQWSSnPlT	WYQQKsGtSPkrwIY FGaGTKLELKR	DTSkLAS 79
1G7	2	DIELTQSPAIMSASPGEKVIMTC QVPaRFSGSGSGTSYSLTISsMEAEDaATYYC	SASS SVSyMh QQWSSnPlT	WYQQKsGtSPkrwIY FGaGTKLELKR	DTSkLAS 80
1A1	2	DIELTQSPASLAVSLGQRATISC GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	RASESVDSYGNSFMG QQWSSYPFT	WYQQKPGQPPKLLIY FGSGTKLELKR	LASNLES 81
1F1	2	DIELTQSPtSLAVSLGQRATISC GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	RASESVDSYGNSFMH QQySgYPlT	WYQQKPGQPPKLLIY FGSGTKLELKR	LASNLES 82
C39	1	DIELTQSPASLAVSLGrRATISC GVPARFSGSGSRTDFTLTIDPVEADDAATYYC	RASESVDSYGhSFMH QQWSSYPlT	WYQQKPGQPPKLLIY FGSGTKLELKR	LASNLES 83
C25	1	DIELTQSPASLAVSLGQRATISC GiPARFSGSGSgTDFTLTInPVEADDvATYYC	RASESVDSYGhSFMq QQWSSYPlT	WYQQKPGQPPKLLIY FGSGTKLELKR	rASNLEp 84
2G5	2	DIELTQSPAimsaSpGekvtttC GVPARFSGSGSgTsysLTIsrmEAeDAATYYC	sASs svSyMG QQsnedPpT	WfQQKPGtsPkLwIY FGSGdqagnKS	stSNLaS 85
3C3	2	DIELTQSPAimsaSpGekvtttC GVPARFSGSGSgTsysLTIsrmEAeDAATYYC	RASESVDSYGhSFMq QQsnedPyT	WfQQKPGtsPkLwIY FGSGdqagnKR	stSNLaS 86
3F4	2	DtELTQSPAimsaSpGekvtttC GVPvRFSGSGSgTsysLTIsrmEAeDAATYYC	sASs svSyMy QQWSSnPlT	WYQQKPGssPrLLIY FGSGTKLELKR	dtSNLaS 87
3H4	2	DIELTQSPAimsaSpGekvtttC GVPvRFSGSGSgTsysLTIsrmEAeDAATYYC	RASsS vssSylG QQWSSnPlT	WYQQKPGssPrLLIY FGSGTKLELKR	dtSNLaS 88
1B3	2	DSELTQSPTTMAASPGEKITTTC GVPARFSGSGSGTSYSLTIGTMEAEDVATYYC	SASSS ISSNYLH QQGSSIPRT	WYQQRPGFSPKLLIY FGGGTKLEIKR	RTSNLAS 89
1C6	2	DiELTQSPaslAvSlGrraTTsC GVPARFSGSGSGTdfSLnIhpvEe DiAmYfC	rASeSveyygtslmq QQsrkvPwT	WYQQkPGqpPKLLIY FGGGTKLEIKR	aaSNveS 90
2B6	2	yiELTQSPaslAvSlGqraTTsC	rASeSvdsygnsfmH	WYQQkPGqpPKLLIY	laSNLeS
		GVPARFSGSGSrTdftLTIdpvEAdDaATYYC	QQnnedPyT	FGGGTKLEIKs	91
1G5	2	DiELTQSPaslAvSlGqraTTsC GaPARFSGSGSGTdfSLnIhpvEedDiAmYfC	rASeSveyygtslmq QQsrkvPyT	WYQQkPGqpPKLLIY FGGGTKLEIKR	aaSNveS 92
1H6	2	DiELTQSPaiMsASPGEKvTTTC GVPvRFSGSGSGTSYSLTIssMEAEDaATYYC	SvSSS ISSsnLH QQwSSyPlT	WYQQksGtSPKLwIY FGaGTKvElrR	gTSNLAS 93
1F3	2	DIELTQSPASMSASPGEKVTMTC GVPSRFSGSGSGTSYLSTISSVEAEDAATYYC	RATSS VSSSYLH QQYIGYPYT	WYQQKSGASPKLWIY FGGGTKLEIKR	SASNLAS 94

2E8	2	DIELTQSPttMaASPGEKiTiTC GVPaRFSGSGSGTSYSLTIgavEAEDvATYYC	sAsSS igSnYLH QQgssiPYT	WYQQKpGfSPKLlIY FGGGTKLEIKR	ktSNLAS 95

[a] Lib, library.

[b] Full-length sequences were not determined for clones C12, C13, C2, and S44 (all bind epitope 1). Accession can be made through GenBank with nos: AF003702 to AF003725.